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1600

#21

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/371,347A

DATE: 06/11/2002

TIME: 10:48:02

RECEIVED

JUN 13 2002

TECH CENTER 1600/2900

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\06112002\I371347A.raw

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4 <110> APPLICANT: Gravel, Roy A,
5   Rozen, Rima
6   Leclerc, Daniel
7   Wilson, Aaron
8   Rosenblatt, David
10 <120> TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:
11   CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE
12   DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER
15 <130> FILE REFERENCE: 50004/003003
17 <140> CURRENT APPLICATION NUMBER: 09/371,347A
18 <141> CURRENT FILING DATE: 1999-08-10
20 <150> PRIOR APPLICATION NUMBER: 09/232,028
21 <151> PRIOR FILING DATE: 1999-01-15
23 <150> PRIOR APPLICATION NUMBER: 60/071,622
24 <151> PRIOR FILING DATE: 1998-01-16
26 <160> NUMBER OF SEQ ID NOS: 61
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2097
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <400> SEQUENCE: 1
36 atgaggaggt ttctgttact atatgctaca cagcagggac aggcaaaggc catcgcagaa 60
37 gaaatgtgtg agcaagctgt ggtacatgga ttttctgcag atcttcactg tattagttaa 120
38 tccgataagt atgacctaaa aaccgaaaca gctcctcttg ttgttggttg ttctaccacg 180
39 ggcaccggag acccaccoga cacagcccgc aagtttgtta aggaaataca gaaccaaaca 240
40 ctgccgggtg atttctttgc tcacctgcgg tatgggttac tgggtctcgg tgattcagaa 300
41 tacacctact ttgcaatgg ggggaagata attgataaac gacttcaaga gcttgaggcc 360
42 cggcatttct atgacactgg acatgcagat gactgtgtag gtttagaact tgtggttgag 420
43 ccgtggattg ctggactctg gccagccctc agaaagcatt ttaggtcaag cagaggacaa 480
44 gaggagataa gtggcgcaact cccgggtggca tcacctgcat ccttgaggac agacctgtg 540
45 aagtcagagc tgctacacat tgaatctcaa gtcgagcttc tgagattcga tgattcagga 600
46 agaaaggatt ctgaggtttt gaagcaaaat gcagtgaaca gcaaccaatc caatgttgta 660
47 attgaagact ttgagtcctc acttaccctg tcggtacccc cactctcaca agcctctctg 720
48 aatattctcg gtttaccctc agaatattta caggtacatc tgcaggagtc tcttgccag 780
49 gaggaagacc aagtatctgt gacttcagca gatccagttt ttcaagtgcc aatttcaaag 840
50 gcagttcaac ttactacgaa tgatgccata aaaaccactc tgctggtaga attggacatt 900
51 tcaaatacag acttttctta tcagcctgga gatgccttca gcgtgatctg ccctaacagt 960
52 gattctgagg tacaaagcct actccaaaaga ctgcagcttg aagataaaaag agagcactgc 1020
53 gtccttttga aaataaaggc agacacaaaag aagaaaggag ctaccttacc ccagcatata 1080
54 cctgcgggat gttctctcca gttcattttt acctggtgtc ttgaaatccg agcaattcct 1140
55 aaaaaggcat ttttgcgagc ccttgtggac tataaccagt acagtgtctga aaagcgcagg 1200
56 ctacaggagc tgtgcagtaa acaaggggca gccgattata gccgctttgt acgagatgcc 1260

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57 tgtgacctgct tgttggatct cctcctcgct ttcccttctt gccagccacc actcagtctc 1320
58 ctgctcgaac atcttcctaa acttcaaccc agaccatatt cgtgtgcaag ctcaagttta 1380
59 tttcaccag gaaagctcca ttttgtcttc aacattgtgg aatttctgtc tactgccaca 1440
60 acagaggttc tgcggaagg agtatgtaca ggctggctgg ccttgttggg tgccttcagtt 1500
61 cttcagccaa acatacatgc atcccatgaa gacagcgga aagccctggc tcctaagata 1560
62 tccatctctc ctggaacaac aaattcttct cacttaccag atgaccctc aatccccatc 1620
63 ataatgggtg gtccaggaac cggcatagcc ccgtttattg gggttcctaca acatagagag 1680
64 aaactccaag aacaacaccc agatggaaat tttggagcaa tgtgggttgg ttttggctgc 1740
65 aggcataagg atagggatta tctattcaga aaagagctca gacatttcct taagcatggg 1800
66 atcttaactc atctaaagggt ttccttctca agagatgctc ctgttgggga ggaggaagcc 1860
67 ccagcaaagt atgtacaaga caacatccag cttcatggcc agcaggtggc gagaatcctc 1920
68 ctccaggaga acggccatat ttatgtgtgt ggagatgcaa agaatatggc caaggatgta 1980
69 catgatgccc ttgtgcaaat aataagcaaa gaggttggag ttgaaaaact agaagcaatg 2040
70 aaaaccctgg ccactttaaa agaagaaaaa cgctaccttc aggatatttg gtcataa 2097

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72 &lt;210&gt; SEQ ID NO: 2

73 &lt;211&gt; LENGTH: 698

74 &lt;212&gt; TYPE: PRT

75 &lt;213&gt; ORGANISM: Homo sapiens

77 &lt;400&gt; SEQUENCE: 2

```

78 Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
79 1 5 10 15
80 Ala Ile Ala Glu Met Cys Glu Gln Ala Val Val His Gly Phe Ser
81 20 25 30
82 Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Tyr Asp Leu Lys Thr
83 35 40 45
84 Glu Thr Ala Pro Leu Val Val Val Ser Thr Thr Gly Thr Gly Asp
85 50 55 60
86 Pro Pro Asp Thr Ala Arg Lys Phe Val Lys Glu Ile Gln Asn Gln Thr
87 65 70 75 80
88 Leu Pro Val Asp Phe Phe Ala His Leu Arg Tyr Gly Leu Leu Gly Leu
89 85 90 95
90 Gly Asp Ser Glu Tyr Thr Tyr Phe Cys Asn Gly Gly Lys Ile Ile Asp
91 100 105 110
92 Lys Arg Leu Gln Glu Leu Gly Ala Arg His Phe Tyr Asp Thr Gly His
93 115 120 125
94 Ala Asp Asp Cys Val Gly Leu Glu Leu Val Val Glu Pro Trp Ile Ala
95 130 135 140
96 Gly Leu Trp Pro Ala Leu Arg Lys His Phe Arg Ser Ser Arg Gly Gln
97 145 150 155 160
98 Glu Glu Ile Ser Gly Ala Leu Pro Val Ala Ser Pro Ala Ser Leu Arg
99 165 170 175
100 Thr Asp Leu Val Lys Ser Glu Leu Leu His Ile Glu Ser Gln Val Glu
101 180 185 190
102 Leu Leu Arg Phe Asp Asp Ser Gly Arg Lys Asp Ser Glu Val Leu Lys
103 195 200 205
104 Gln Asn Ala Val Asn Ser Asn Gln Ser Asn Val Val Ile Glu Asp Phe
105 210 215 220
106 Glu Ser Ser Leu Thr Arg Ser Val Pro Pro Leu Ser Gln Ala Ser Leu
107 225 230 235 240

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```

108 Asn Ile Pro Gly Leu Pro Pro Glu Tyr Leu Gln Val His Leu Gln Glu
109                245                250                255
110 Ser Leu Gly Gln Glu Glu Ser Gln Val Ser Val Thr Ser Ala Asp Pro
111                260                265                270
112 Val Phe Gln Val Pro Ile Ser Lys Ala Val Gln Leu Thr Thr Asn Asp
113                275                280                285
114 Ala Ile Lys Thr Thr Leu Leu Val Glu Leu Asp Ile Ser Asn Thr Asp
115                290                295                300
116 Phe Ser Tyr Gln Pro Gly Asp Ala Phe Ser Val Ile Cys Pro Asn Ser
117 305                310                315                320
118 Asp Ser Glu Val Gln Ser Leu Leu Gln Arg Leu Gln Leu Glu Asp Lys
119                325                330                335
120 Arg Glu His Cys Val Leu Leu Lys Ile Lys Ala Asp Thr Lys Lys Lys
121                340                345                350
122 Gly Ala Thr Leu Pro Gln His Ile Pro Ala Gly Cys Ser Leu Gln Phe
123                355                360                365
124 Ile Phe Thr Trp Cys Leu Glu Ile Arg Ala Ile Pro Lys Lys Ala Phe
125                370                375                380
126 Leu Arg Ala Leu Val Asp Tyr Thr Ser Asp Ser Ala Glu Lys Arg Arg
127 385                390                395                400
128 Leu Gln Glu Leu Cys Ser Lys Gln Gly Ala Ala Asp Tyr Ser Arg Phe
129                405                410                415
130 Val Arg Asp Ala Cys Ala Cys Leu Leu Asp Leu Leu Leu Ala Phe Pro
131                420                425                430
132 Ser Cys Gln Pro Pro Leu Ser Leu Leu Glu His Leu Pro Lys Leu
133                435                440                445
134 Gln Pro Arg Pro Tyr Ser Cys Ala Ser Ser Ser Leu Phe His Pro Gly
135                450                455                460
136 Lys Leu His Phe Val Phe Asn Ile Val Glu Phe Leu Ser Thr Ala Thr
137 465                470                475                480
138 Thr Glu Val Leu Arg Lys Gly Val Cys Thr Gly Trp Leu Ala Leu Leu
139                485                490                495
140 Val Ala Ser Val Leu Gln Pro Asn Ile His Ala Ser His Glu Asp Ser
141                500                505                510
142 Gly Lys Ala Leu Ala Pro Lys Ile Ser Ile Ser Pro Arg Thr Thr Asn
143                515                520                525
144 Ser Phe His Leu Pro Asp Asp Pro Ser Ile Pro Ile Ile Met Val Gly
145                530                535                540
146 Pro Gly Thr Gly Ile Ala Pro Phe Ile Gly Phe Leu Gln His Arg Glu
147 545                550                555                560
148 Lys Leu Gln Glu Gln His Pro Asp Gly Asn Phe Gly Ala Met Trp Leu
149                565                570                575
150 Phe Phe Gly Cys Arg His Lys Asp Arg Asp Tyr Leu Phe Arg Lys Glu
151                580                585                590
152 Leu Arg His Phe Leu Lys His Gly Ile Leu Thr His Leu Lys Val Ser
153                595                600                605
154 Phe Ser Arg Asp Ala Pro Val Gly Glu Glu Glu Ala Pro Ala Lys Tyr
155                610                615                620
156 Val Gln Asp Asn Ile Gln Leu His Gly Gln Gln Val Ala Arg Ile Leu

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```

157 625          630          635          640
158 Leu Gln Glu Asn Gly His Ile Tyr Val Cys Gly Asp Ala Lys Asn Met
159          645          650          655
160 Ala Lys Asp Val His Asp Ala Leu Val Gln Ile Ile Ser Lys Glu Val
161          660          665          670
162 Gly Val Glu Lys Leu Glu Ala Met Lys Thr Leu Ala Thr Leu Lys Glu
163          675          680          685
164 Glu Lys Arg Tyr Leu Gln Asp Ile Trp Ser
165          690          695
168 <210> SEQ ID NO: 3
169 <211> LENGTH: 24
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
173 <400> SEQUENCE: 3
174 ctctgtctcg aacatcttcc taaa                24
176 <210> SEQ ID NO: 4
177 <211> LENGTH: 25
178 <212> TYPE: DNA
179 <213> ORGANISM: Homo sapiens
181 <400> SEQUENCE: 4
182 aatagataat ccctatcctt atgcc                25
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 23
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 5
190 ccctggctcc taagatatcc atc                23
192 <210> SEQ ID NO: 6
193 <211> LENGTH: 26
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 6
198 cgaacaacaa attctttcca cttacc                26
200 <210> SEQ ID NO: 7
201 <211> LENGTH: 23
202 <212> TYPE: DNA
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 7
206 caagggttgg ggaagtcgcg ttg                23
208 <210> SEQ ID NO: 8
209 <211> LENGTH: 25
210 <212> TYPE: DNA
211 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 8
214 atgccttgaa gtgatgagga ggttt                25
216 <210> SEQ ID NO: 9
217 <211> LENGTH: 24
218 <212> TYPE: DNA
219 <213> ORGANISM: Homo sapiens

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221 <400> SEQUENCE: 9
222 ttcctacaac atagagagaa actc 24
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 24
226 <212> TYPE: DNA
227 <213> ORGANISM: Homo sapiens
229 <400> SEQUENCE: 10
230 ttgcacaagg gcatcatgta catc 24
232 <210> SEQ ID NO: 11
233 <211> LENGTH: 25
234 <212> TYPE: DNA
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 11
238 aaacctcctc atcacttcaa ggcac 25
240 <210> SEQ ID NO: 12
241 <211> LENGTH: 23
242 <212> TYPE: DNA
243 <213> ORGANISM: Homo sapiens
245 <400> SEQUENCE: 12
246 ctgtcacacg aatatggtct ggg 23
248 <210> SEQ ID NO: 13
249 <211> LENGTH: 23
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapiens
253 <400> SEQUENCE: 13
254 tggcatcacc tgcacacctg agg 23
256 <210> SEQ ID NO: 14
257 <211> LENGTH: 25
258 <212> TYPE: DNA
259 <213> ORGANISM: Homo sapiens
261 <400> SEQUENCE: 14
262 gatgtacctg taaatattct ggggg 25
264 <210> SEQ ID NO: 15
265 <211> LENGTH: 24
266 <212> TYPE: DNA
267 <213> ORGANISM: Homo sapiens
269 <400> SEQUENCE: 15
270 aatccacggc tcaaccacaa gtgc 24
272 <210> SEQ ID NO: 16
273 <211> LENGTH: 25
274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <400> SEQUENCE: 16
278 ctcgaaatta accctcacta aaggg 25
280 <210> SEQ ID NO: 17
281 <211> LENGTH: 23
282 <212> TYPE: DNA
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 17

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**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/09/371,347A**

**DATE: 06/11/2002**

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**Input Set : A:\PTO.AMC.txt**

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